

OM protein - protein search, using sw model

Run on: April 13, 2006, 10:09:13 ; Search time 189 Seconds
 (without alignments)
 30.222 Million cell updates/sec

Title: US-10-784-589A-29
 Perfect score: 82
 Sequence: 1 EIEWYSWVTHGMY 13

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_21:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	82	100.0	13	4	AAU07827	Aau07827 Peptide i
2	82	100.0	16	4	AAU07804	Aau07804 Peptide #
3	82	100.0	16	4	AAU07812	Aau07812 Peptide i
4	82	100.0	16	4	AAU07811	Aau07811 Peptide i
5	82	100.0	16	4	AAU07801	Aau07801 Peptide #
6	82	100.0	16	9	ADV87369	Adv87369 Flt1 tyro
7	82	100.0	17	4	AAU07803	Aau07803 Peptide #
8	82	100.0	17	4	AAU07802	Aau07802 Peptide #

9	82	100.0	19	4	AAU07805	Aau07805	Peptide #
10	79	96.3	16	4	AAU07818	Aau07818	Peptide i
11	77	93.9	15	4	AAU07806	Aau07806	Peptide #
12	77	93.9	16	4	AAU07814	Aau07814	Peptide i
13	77	93.9	16	4	AAU07820	Aau07820	Peptide i
14	77	93.9	16	4	AAU07808	Aau07808	Peptide e
15	77	93.9	16	4	AAU07813	Aau07813	Peptide i
16	76	92.7	16	4	AAU07815	Aau07815	Peptide i
17	76	92.7	16	4	AAU07822	Aau07822	Peptide i
18	75	91.5	16	4	AAU07823	Aau07823	Peptide i
19	73	89.0	16	4	AAU07817	Aau07817	Peptide i
20	72	87.8	16	4	AAU07821	Aau07821	Peptide i
21	71	86.6	16	4	AAU07824	Aau07824	Peptide i
22	68	82.9	16	4	AAU07816	Aau07816	Peptide i
23	68	82.9	16	4	AAU07819	Aau07819	Peptide i
24	54	65.9	16	4	AAU07825	Aau07825	Peptide i
25	48	58.5	632	8	ADS11946	Ads11946	Human the
26	48	58.5	632	8	ADS11947	Ads11947	Human the
27	48	58.5	632	8	ADS11945	Ads11945	Human the
28	48	58.5	647	8	ADS10679	Ads10679	Human the
29	47	57.3	7	4	AAU07826	Aau07826	Peptide i
30	43	52.4	52	8	ABO57201	Abo57201	Human gen
31	43	52.4	82	7	ADH86156	Adh86156	Enterococ
32	43	52.4	266	9	AEB39581	Aeb39581	L. pneumo
33	43	52.4	271	9	AEB36158	Aeb36158	L. pneumo
34	43	52.4	489	8	ADY08745	Ady08745	Plant ful
35	43	52.4	541	8	ADT50292	Adt50292	Euglena g
36	43	52.4	541	9	ADW96411	Adw96411	Euglena g
37	43	52.4	662	4	AAE00939	Aae00939	Human 15S
38	43	52.4	662	7	ADD47873	Add47873	Human Pro
39	43	52.4	662	8	ADJ75368	Adj75368	Marker ge
40	43	52.4	662	8	ADQ91786	Adq91786	Human 15S
41	43	52.4	662	8	ADQ37894	Adq37894	Human 15-
42	43	52.4	684	5	ABB08005	Abb08005	Human lip
43	42.5	51.8	57	4	AAM30997	Aam30997	Peptide #
44	42.5	51.8	57	4	ABG52390	Abg52390	Human liv
45	42.5	51.8	57	5	ABG40399	Abg40399	Human pep
46	42.5	51.8	924	4	ABB65189	Abb65189	Drosophil
47	42	51.2	320	8	ADS30364	Ads30364	Bacterial
48	42	51.2	332	9	ABM91606	Abm91606	M. xanthu
49	42	51.2	398	9	ABM92541	Abm92541	M. xanthu
50	42	51.2	1237	8	ABO59715	Abo59715	Human gen
51	42	51.2	2080	8	ABM82284	Abm82284	Tumour-as
52	42	51.2	2098	7	ADG42153	Adg42153	Human bra
53	42	51.2	3234	5	ABP70132	Abp70132	Human NOV
54	42	51.2	3680	4	ABG22108	Abg22108	Novel hum
55	41	50.0	57	4	AAU62183	Aau62183	Propionib
56	41	50.0	57	6	ABM58702	Abm58702	Propionib
57	41	50.0	192	9	ADX40538	Adx40538	HIV Vif p
58	41	50.0	196	6	ADA56825	Ada56825	Human sec
59	41	50.0	196	6	ADA40675	Ada40675	Human sec
60	41	50.0	196	6	ABR47690	Abr47690	Human sec
61	41	50.0	196	7	ADC74069	Adc74069	Human sec
62	41	50.0	197	2	AAY36278	Aay36278	Human sec
63	41	50.0	197	6	ADA11635	Ada11635	Human nov
64	41	50.0	232	3	AAY53630	Aay53630	A bone ma
65	41	50.0	283	6	ABM70292	Abm70292	Photorhab

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OM protein - protein search, using sw model

Run on: April 13, 2006, 10:17:28 ; Search time 48 Seconds
(without alignments)
22.391 Million cell updates/sec

Title: US-10-784-589A-29
Perfect score: 82
Sequence: 1 EIEWYSWVTHGMY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match	Length				
1	82	100.0	13	2	US-09-775-743C-29	Sequence 29, Appl	
2	82	100.0	16	2	US-09-775-743C-1	Sequence 1, Appli	
3	82	100.0	16	2	US-09-775-743C-4	Sequence 4, Appli	
4	82	100.0	16	2	US-09-775-743C-14	Sequence 14, Appl	
5	82	100.0	17	2	US-09-775-743C-2	Sequence 2, Appli	
6	82	100.0	17	2	US-09-775-743C-3	Sequence 3, Appli	
7	82	100.0	19	2	US-09-775-743C-5	Sequence 5, Appli	
8	79	96.3	16	2	US-09-775-743C-20	Sequence 20, Appl	
9	77	93.9	15	2	US-09-775-743C-6	Sequence 6, Appli	
10	77	93.9	16	2	US-09-775-743C-15	Sequence 15, Appl	
11	77	93.9	16	2	US-09-775-743C-16	Sequence 16, Appl	

12	77	93.9	16	2	US-09-775-743C-22	Sequence 22, Appl
13	76	92.7	16	2	US-09-775-743C-17	Sequence 17, Appl
14	76	92.7	16	2	US-09-775-743C-24	Sequence 24, Appl
15	75	91.5	16	2	US-09-775-743C-25	Sequence 25, Appl
16	73	89.0	16	2	US-09-775-743C-19	Sequence 19, Appl
17	72	87.8	16	2	US-09-775-743C-23	Sequence 23, Appl
18	71	86.6	16	2	US-09-775-743C-26	Sequence 26, Appl
19	68	82.9	16	2	US-09-775-743C-18	Sequence 18, Appl
20	68	82.9	16	2	US-09-775-743C-21	Sequence 21, Appl
21	54	65.9	16	2	US-09-775-743C-27	Sequence 27, Appl
22	47	57.3	7	2	US-09-775-743C-28	Sequence 28, Appl
23	44	53.7	232	2	US-09-248-796A-16925	Sequence 16925, A
24	44	53.7	695	2	US-09-248-796A-20895	Sequence 20895, A
25	43	52.4	82	2	US-09-134-000C-4041	Sequence 4041, Ap
26	43	52.4	662	2	US-09-061-768A-25	Sequence 25, Appl
27	43	52.4	662	2	US-09-764-246-25	Sequence 25, Appl
28	43	52.4	662	2	US-09-949-002-315	Sequence 315, App
29	42	51.2	332	2	US-09-902-540-10805	Sequence 10805, A
30	42	51.2	398	2	US-09-902-540-11740	Sequence 11740, A
31	41	50.0	194	2	US-09-270-767-37807	Sequence 37807, A
32	41	50.0	194	2	US-09-270-767-53024	Sequence 53024, A
33	41	50.0	674	2	US-09-949-016-7196	Sequence 7196, Ap
34	41	50.0	2556	1	US-08-185-432-17	Sequence 17, Appl
35	41	50.0	2556	2	US-08-899-232-2	Sequence 2, Appli
36	41	50.0	2556	2	US-09-121-457-2	Sequence 2, Appli
37	40.5	49.4	334	2	US-08-883-526-4	Sequence 4, Appli
38	40.5	49.4	334	2	US-09-519-283-4	Sequence 4, Appli
39	40	48.8	52	2	US-09-621-976-7409	Sequence 7409, Ap
40	40	48.8	65	2	US-09-513-999C-7605	Sequence 7605, Ap
41	40	48.8	221	2	US-09-712-363-211	Sequence 211, App
42	40	48.8	462	2	US-09-328-352-5497	Sequence 5497, Ap
43	40	48.8	540	2	US-09-252-991A-18967	Sequence 18967, A
44	40	48.8	663	2	US-09-641-638-653	Sequence 653, App
45	40	48.8	663	2	US-10-170-097-653	Sequence 653, App
46	40	48.8	663	2	US-09-949-002-306	Sequence 306, App
47	40	48.8	680	2	US-09-949-002-500	Sequence 500, App
48	39.5	48.2	265	2	US-09-198-452A-945	Sequence 945, App
49	39.5	48.2	273	2	US-09-438-185A-881	Sequence 881, App
50	39.5	48.2	320	2	US-08-909-125-4	Sequence 4, Appli
51	39	47.6	66	2	US-09-489-039A-12901	Sequence 12901, A
52	39	47.6	138	2	US-09-710-279-1316	Sequence 1316, Ap
53	39	47.6	163	2	US-10-104-047-1997	Sequence 1997, Ap
54	39	47.6	173	2	US-09-270-767-41340	Sequence 41340, A
55	39	47.6	173	2	US-09-270-767-56556	Sequence 56556, A
56	39	47.6	173	2	US-09-637-746-2	Sequence 2, Appli
57	39	47.6	173	2	US-09-637-746-10	Sequence 10, Appl
58	39	47.6	199	2	US-09-134-001C-3825	Sequence 3825, Ap
59	39	47.6	207	2	US-09-270-767-36201	Sequence 36201, A
60	39	47.6	207	2	US-09-270-767-51418	Sequence 51418, A
61	39	47.6	216	1	US-08-562-985A-6	Sequence 6, Appli
62	39	47.6	443	2	US-09-902-540-14507	Sequence 14507, A
63	39	47.6	482	1	US-08-135-510-5	Sequence 5, Appli
64	39	47.6	482	1	US-08-483-852-5	Sequence 5, Appli
65	39	47.6	482	1	US-08-477-953-5	Sequence 5, Appli
66	39	47.6	482	1	US-08-477-952-5	Sequence 5, Appli
67	39	47.6	499	2	US-09-489-039A-8830	Sequence 8830, Ap
68	39	47.6	503	1	US-08-135-511-29	Sequence 29, Appl

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OM protein - protein search, using sw model

Run on: April 13, 2006, 10:28:43 ; Search time 164 Seconds
(without alignments)
33.121 Million cell updates/sec

Title: US-10-784-589A-29
Perfect score: 82
Sequence: 1 EIEWYSWVTHGMY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	82	100.0	13	5	US-10-784-589-29	Sequence 29, Appl
2	82	100.0	16	3	US-09-775-743A-1	Sequence 1, Appli
3	82	100.0	16	3	US-09-775-743A-4	Sequence 4, Appli
4	82	100.0	16	5	US-10-784-589-1	Sequence 1, Appli
5	82	100.0	16	5	US-10-784-589-4	Sequence 4, Appli
6	82	100.0	16	5	US-10-784-589-14	Sequence 14, Appl
7	82	100.0	17	3	US-09-775-743A-2	Sequence 2, Appli
8	82	100.0	17	3	US-09-775-743A-3	Sequence 3, Appli
9	82	100.0	17	5	US-10-784-589-2	Sequence 2, Appli
10	82	100.0	17	5	US-10-784-589-3	Sequence 3, Appli
11	82	100.0	19	3	US-09-775-743A-5	Sequence 5, Appli

12	82	100.0	19	5	US-10-784-589-5	Sequence 5, Appli
13	79	96.3	16	5	US-10-784-589-20	Sequence 20, Appl
14	77	93.9	15	3	US-09-775-743A-6	Sequence 6, Appli
15	77	93.9	15	5	US-10-784-589-6	Sequence 6, Appli
16	77	93.9	16	5	US-10-784-589-15	Sequence 15, Appl
17	77	93.9	16	5	US-10-784-589-16	Sequence 16, Appl
18	77	93.9	16	5	US-10-784-589-22	Sequence 22, Appl
19	76	92.7	16	5	US-10-784-589-17	Sequence 17, Appl
20	76	92.7	16	5	US-10-784-589-24	Sequence 24, Appl
21	75	91.5	16	5	US-10-784-589-25	Sequence 25, Appl
22	73	89.0	16	5	US-10-784-589-19	Sequence 19, Appl
23	72	87.8	16	5	US-10-784-589-23	Sequence 23, Appl
24	71	86.6	16	5	US-10-784-589-26	Sequence 26, Appl
25	68	82.9	16	5	US-10-784-589-18	Sequence 18, Appl
26	68	82.9	16	5	US-10-784-589-21	Sequence 21, Appl
27	54	65.9	16	5	US-10-784-589-27	Sequence 27, Appl
28	47	57.3	7	5	US-10-784-589-28	Sequence 28, Appl
29	46.5	56.7	149	4	US-10-425-115-297392	Sequence 297392,
30	46	56.1	47	4	US-10-425-115-318461	Sequence 318461,
31	44	53.7	160	4	US-10-425-115-260390	Sequence 260390,
32	44	53.7	194	4	US-10-767-701-40133	Sequence 40133, A
33	43	52.4	52	4	US-10-029-386-30835	Sequence 30835, A
34	43	52.4	489	4	US-10-425-114-64560	Sequence 64560, A
35	43	52.4	562	4	US-10-425-115-267281	Sequence 267281,
36	43	52.4	661	5	US-10-688-676A-2	Sequence 2, Appli
37	43	52.4	662	3	US-09-764-246-25	Sequence 25, Appl
38	43	52.4	662	4	US-10-716-204-25	Sequence 25, Appl
39	43	52.4	662	5	US-10-631-467-620	Sequence 620, App
40	43	52.4	669	4	US-10-437-963-169798	Sequence 169798,
41	43	52.4	684	4	US-10-398-663-5	Sequence 5, Appli
42	43	52.4	1062	4	US-10-437-963-120734	Sequence 120734,
43	42.5	51.8	57	3	US-09-864-761-46785	Sequence 46785, A
44	42.5	51.8	924	6	US-11-097-143-22359	Sequence 22359, A
45	42	51.2	90	4	US-10-767-701-59497	Sequence 59497, A
46	42	51.2	297	4	US-10-156-761-9970	Sequence 9970, Ap
47	42	51.2	320	4	US-10-369-493-19397	Sequence 19397, A
48	42	51.2	1237	4	US-10-029-386-33349	Sequence 33349, A
49	42	51.2	3234	4	US-10-093-463-168	Sequence 168, App
50	42	51.2	3680	5	US-10-450-763-52467	Sequence 52467, A
51	41	50.0	45	4	US-10-425-115-351272	Sequence 351272,
52	41	50.0	94	4	US-10-425-115-209126	Sequence 209126,
53	41	50.0	197	4	US-10-097-065-163	Sequence 163, App
54	41	50.0	197	4	US-10-372-876-163	Sequence 163, App
55	41	50.0	232	3	US-09-765-205-18	Sequence 18, Appl
56	41	50.0	232	5	US-10-347-669-18	Sequence 18, Appl
57	41	50.0	279	4	US-10-437-963-151212	Sequence 151212,
58	41	50.0	292	4	US-10-425-114-67472	Sequence 67472, A
59	41	50.0	319	4	US-10-369-493-8124	Sequence 8124, Ap
60	41	50.0	433	4	US-10-425-115-330467	Sequence 330467,
61	41	50.0	434	5	US-10-870-492-74	Sequence 74, Appl
62	41	50.0	438	4	US-10-425-114-66753	Sequence 66753, A
63	41	50.0	547	4	US-10-270-333-198	Sequence 198, App
64	41	50.0	547	6	US-11-097-143-42831	Sequence 42831, A
65	41	50.0	579	5	US-10-489-425-58	Sequence 58, Appl
66	41	50.0	669	5	US-10-482-029-86	Sequence 86, Appl
67	41	50.0	686	4	US-10-408-765A-1545	Sequence 1545, Ap
68	40.5	49.4	334	3	US-09-519-283-4	Sequence 4, Appli

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OM protein - protein search, using sw model

Run on: April 13, 2006, 10:29:38 ; Search time 26 Seconds
(without alignments)
21.245 Million cell updates/sec

Title: US-10-784-589A-29
Perfect score: 82
Sequence: 1 EIEWYSWVTHGMY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match	Length				
1	43	52.4	456	7	US-11-096-568A-19227	Sequence 19227, A	
2	43	52.4	458	7	US-11-096-568A-19226	Sequence 19226, A	
3	43	52.4	467	7	US-11-096-568A-19225	Sequence 19225, A	
4	43	52.4	541	7	US-11-112-882-34	Sequence 34, Appl	
5	43	52.4	541	7	US-11-146-428-75	Sequence 75, Appl	
6	42	51.2	2080	7	US-11-124-367A-364	Sequence 364, App	
7	42	51.2	2542	7	US-11-124-367A-363	Sequence 363, App	
8	41	50.0	334	7	US-11-087-099-3986	Sequence 3986, Ap	
9	40.5	49.4	334	6	US-10-663-053-4	Sequence 4, Appli	

10	40	48.8	89	6	US-10-925-366A-342	Sequence 342, App
11	40	48.8	89	7	US-11-098-758-342	Sequence 342, App
12	40	48.8	118	7	US-11-049-536-334	Sequence 334, App
13	40	48.8	118	7	US-11-199-739-334	Sequence 334, App
14	40	48.8	118	7	US-11-217-919-156	Sequence 156, App
15	40	48.8	245	7	US-11-096-568A-28422	Sequence 28422, A
16	40	48.8	369	7	US-11-087-099-7804	Sequence 7804, Ap
17	40	48.8	459	7	US-11-096-568A-28421	Sequence 28421, A
18	39	47.6	138	6	US-10-793-626-1316	Sequence 1316, Ap
19	39	47.6	163	7	US-11-072-512-1997	Sequence 1997, Ap
20	38.5	47.0	123	7	US-11-102-512-58	Sequence 58, Appl
21	38	46.3	118	7	US-11-206-587-33	Sequence 33, Appl
22	38	46.3	259	7	US-11-056-825-7	Sequence 7, Appli
23	38	46.3	261	7	US-11-056-825-2	Sequence 2, Appli
24	38	46.3	394	7	US-11-087-099-10247	Sequence 10247, A
25	38	46.3	443	7	US-11-087-099-2772	Sequence 2772, Ap
26	38	46.3	454	7	US-11-087-099-6741	Sequence 6741, Ap
27	38	46.3	455	7	US-11-087-099-4243	Sequence 4243, Ap
28	38	46.3	471	7	US-11-087-099-5984	Sequence 5984, Ap
29	38	46.3	472	7	US-11-087-099-3650	Sequence 3650, Ap
30	38	46.3	478	7	US-11-188-298-10347	Sequence 10347, A
31	38	46.3	497	7	US-11-087-099-4483	Sequence 4483, Ap
32	38	46.3	498	7	US-11-188-298-1542	Sequence 1542, Ap
33	38	46.3	498	7	US-11-188-298-15514	Sequence 15514, A
34	38	46.3	499	7	US-11-188-298-2126	Sequence 2126, Ap
35	38	46.3	499	7	US-11-188-298-3160	Sequence 3160, Ap
36	38	46.3	499	7	US-11-188-298-9964	Sequence 9964, Ap
37	38	46.3	499	7	US-11-188-298-10118	Sequence 10118, A
38	38	46.3	499	7	US-11-188-298-10150	Sequence 10150, A
39	38	46.3	499	7	US-11-188-298-14405	Sequence 14405, A
40	38	46.3	499	7	US-11-188-298-18937	Sequence 18937, A
41	38	46.3	522	7	US-11-087-099-284	Sequence 284, App
42	38	46.3	549	7	US-11-087-099-6201	Sequence 6201, Ap
43	38	46.3	550	7	US-11-087-099-8310	Sequence 8310, Ap
44	38	46.3	579	7	US-11-188-298-20145	Sequence 20145, A
45	38	46.3	592	7	US-11-188-298-18244	Sequence 18244, A
46	37	45.1	250	7	US-11-054-515-1348	Sequence 1348, Ap
47	37	45.1	250	7	US-11-266-444-1348	Sequence 1348, Ap
48	37	45.1	251	7	US-11-054-515-258	Sequence 258, App
49	37	45.1	251	7	US-11-054-515-310	Sequence 310, App
50	37	45.1	251	7	US-11-266-444-258	Sequence 258, App
51	37	45.1	251	7	US-11-266-444-310	Sequence 310, App
52	37	45.1	264	6	US-10-506-454-1689	Sequence 1689, Ap
53	37	45.1	283	7	US-11-070-723A-6	Sequence 6, Appli
54	37	45.1	284	7	US-11-070-723A-8	Sequence 8, Appli
55	37	45.1	284	7	US-11-070-723A-46	Sequence 46, Appl
56	37	45.1	288	7	US-11-070-723A-12	Sequence 12, Appl
57	37	45.1	294	7	US-11-096-568A-3682	Sequence 3682, Ap
58	37	45.1	297	7	US-11-070-723A-10	Sequence 10, Appl
59	37	45.1	312	7	US-11-096-568A-3681	Sequence 3681, Ap
60	37	45.1	457	7	US-11-087-099-1034	Sequence 1034, Ap
61	37	45.1	457	7	US-11-188-298-11990	Sequence 11990, A
62	37	45.1	467	7	US-11-087-099-803	Sequence 803, App
63	37	45.1	469	7	US-11-087-099-11442	Sequence 11442, A
64	37	45.1	469	7	US-11-188-298-10552	Sequence 10552, A
65	37	45.1	470	7	US-11-087-099-4467	Sequence 4467, Ap
66	37	45.1	470	7	US-11-087-099-4643	Sequence 4643, Ap

OM protein - protein search, using sw model

Run on: April 13, 2006, 10:13:38 ; Search time 40 Seconds
 (without alignments)
 31.270 Million cell updates/sec

Title: US-10-784-589A-29
 Perfect score: 82
 Sequence: 1 EIEWYSWVTHGM 13

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	44.5	54.3	152	2	G75123	hypothetical prote
2	43	52.4	618	2	T24228	hypothetical prote
3	43	52.4	662	1	A31349	arachidonate 15-li
4	43	52.4	663	2	S32825	arachidonate 12-li
5	43	52.4	864	2	JC4624	alpha-glucosidase
6	43	52.4	958	1	P1BVCC	1a protein - cowpe
7	42	51.2	166	2	T34229	hypothetical prote
8	41	50.0	148	2	T49732	hypothetical prote
9	41	50.0	283	2	D72378	sugar ABC transpor
10	41	50.0	434	2	T16080	hypothetical prote
11	41	50.0	442	2	S50332	NADH2 dehydrogenas
12	41	50.0	552	2	S45886	hypothetical prote
13	41	50.0	579	2	JC7896	corazonin receptor

14	41	50.0	814	2	T33140	hypothetical prote
15	41	50.0	1661	2	T31330	head-activator bin
16	40.5	49.4	334	2	A58195	cathepsin L (EC 3.
17	40.5	49.4	516	2	G82182	probable NADH dehy
18	40	48.8	100	2	D71632	hypothetical prote
19	40	48.8	221	2	B70890	hypothetical prote
20	40	48.8	307	2	AE0962	D-serine deaminase
21	40	48.8	311	2	A65010	D-serine deaminase
22	40	48.8	333	2	T19889	hypothetical prote
23	40	48.8	370	2	S54297	protein phosphatas
24	40	48.8	422	2	T49513	gastric mucin rela
25	40	48.8	435	2	D82955	probable MFS dicar
26	40	48.8	443	2	AD3050	MFS permease [alph
27	40	48.8	477	2	H98235	probable mfs dicar
28	40	48.8	477	2	G87375	major facilitator
29	40	48.8	566	2	A83832	glycine betaine tr
30	40	48.8	650	2	B87791	protein B0207.1 [i
31	40	48.8	663	1	A35087	arachidonate 12-li
32	40	48.8	663	1	A38283	arachidonate 12-li
33	40	48.8	671	2	A56592	NADPH-ferrihemopro
34	40	48.8	941	2	T32449	hypothetical prote
35	40	48.8	966	1	P1BVBB	RNA la protein - b
36	40	48.8	1258	2	T40737	probable calcium-t
37	39.5	48.2	214	2	G83692	hypothetical prote
38	39.5	48.2	265	2	E86600	metal dependent hy
39	39.5	48.2	265	2	E72024	metal dependent hy
40	39	47.6	184	2	F89969	conserved hypothet
41	39	47.6	279	2	T37010	probable DNA-bindi
42	39	47.6	325	2	E69806	conserved hypothet
43	39	47.6	349	2	T15422	hypothetical prote
44	39	47.6	353	2	S37873	hypothetical prote
45	39	47.6	365	2	C97735	hypothetical prote
46	39	47.6	501	2	I46701	cholesterol 7alpha
47	39	47.6	503	1	A35376	cholesterol 7alpha
48	39	47.6	504	1	JH0659	cholesterol 7alpha
49	39	47.6	504	2	S39399	cholesterol 7alpha
50	39	47.6	537	2	H88087	protein B0454.4 [i
51	39	47.6	663	1	A54075	arachidonate 12-li
52	39	47.6	877	2	G70934	hypothetical prote
53	39	47.6	1118	1	A49724	protein-tyrosine-p
54	38	46.3	118	2	G37267	Ig heavy chain V r
55	38	46.3	162	2	S76809	hypothetical prote
56	38	46.3	174	2	I54543	MHC class I histoc
57	38	46.3	194	2	A69760	conserved hypothet
58	38	46.3	198	2	H90550	hypothetical prote
59	38	46.3	247	2	D72562	hypothetical prote
60	38	46.3	254	2	T15952	hypothetical prote
61	38	46.3	261	2	G86880	hypothetical prote
62	38	46.3	274	2	E97202	hypothetical prote
63	38	46.3	278	2	AF2895	hypothetical prote
64	38	46.3	300	2	B89850	hypothetical prote
65	38	46.3	300	2	AF1286	CDP-abequose synth
66	38	46.3	300	2	AI1657	CDP-abequose synth
67	38	46.3	302	2	S50579	hypothetical prote
68	38	46.3	314	2	B83487	hypothetical prote
69	38	46.3	324	2	G82410	transcription regu
70	38	46.3	338	2	T17374	NADH2 dehydrogenas

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OM protein - protein search, using sw model

Run on: April 13, 2006, 10:09:43 ; Search time 229 Seconds
(without alignments)
40.052 Million cell updates/sec

Title: US-10-784-589A-29
Perfect score: 82
Sequence: 1 EIEWYSWVTHGMY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	47	57.3	261	2	Q5FNF8_GLUOX	Q5fnf8 gluconobact
2	47	57.3	342	2	Q66IY2_XENLA	Q66iy2 xenopus lae
3	47	57.3	384	2	Q5FN87_GLUOX	Q5fn87 gluconobact
4	46	56.1	49	2	Q66266_9BROM	Q66266 cucumber mo
5	46	56.1	342	2	Q6DFQ7_XENTR	Q6dfq7 xenopus tro
6	45	54.9	129	2	Q4RP80_TETNG	Q4rp80 tetraodon n
7	45	54.9	209	2	Q88T96_LACPL	Q88t96 lactobacill
8	45	54.9	212	2	Q5D916_SCHJA	Q5d916 schistosoma
9	45	54.9	290	2	Q9IK76_NPVST	Q9ik76 spodoptera
10	45	54.9	662	1	LX12E_MOUSE	P55249 mus musculu
11	45	54.9	662	2	Q5E901_MOUSE	Q5e901 mus musculu
12	44.5	54.3	152	2	Q9V0J9_PYRAB	Q9v0j9 pyrococcus
13	44	53.7	147	2	Q4Q4R1_LEIMA	Q4q4r1 leishmania
14	44	53.7	463	2	Q5KRB5_CORGL	Q5krb5 corynebacte
15	44	53.7	466	2	Q4NIB5_9MICC	Q4nib5 arthrobacte

16	44	53.7	514	2	Q5B5N1_EMENI	Q5b5n1	aspergillus
17	44	53.7	534	2	Q4RYF1_TETNG	Q4ryf1	tetraodon n
18	44	53.7	593	2	Q6AMX4_DESPS	Q6amx4	desulfotale
19	44	53.7	684	2	Q5A2B5_CANAL	Q5a2b5	candida alb
20	44	53.7	954	2	Q4I4W2_GIBZE	Q4i4w2	gibberella
21	43	52.4	227	2	Q4P3K8_USTMA	Q4p3k8	ustilago ma
22	43	52.4	266	2	Q5WU23_LEGPL	Q5wu23	legionella
23	43	52.4	266	2	Q5X2A2_LEGPA	Q5x2a2	legionella
24	43	52.4	268	2	Q5ZSU1_LEGPH	Q5zsu1	legionella
25	43	52.4	337	2	Q6SHT7_9BACT	Q6sht7	uncultured
26	43	52.4	425	2	Q618S1_CAEBR	Q618s1	caenorhabdi
27	43	52.4	454	2	Q5QLC0_ORYSA	Q5qlc0	oryza sativ
28	43	52.4	501	2	Q7SHL0_NEUCR	Q7shl0	neurospora
29	43	52.4	541	2	Q6WNG7_EUGGR	Q6wng7	euglena gra
30	43	52.4	600	2	Q61ZJ7_CAEBR	Q61zj7	caenorhabdi
31	43	52.4	601	2	Q61H01_CAEBR	Q61h01	caenorhabdi
32	43	52.4	602	2	Q966P8_CAEEL	Q966p8	caenorhabdi
33	43	52.4	618	2	Q22003_CAEEL	Q22003	caenorhabdi
34	43	52.4	661	1	LOX15_HUMAN	P16050	homo sapien
35	43	52.4	661	1	LOX15_PONPY	Q5rbe8	pongo pygma
36	43	52.4	662	1	LOX12_BOVIN	P27479	bos taurus
37	43	52.4	836	2	Q4IQY7_GIBZE	Q4iqy7	gibberella
38	43	52.4	840	2	Q4WX15_ASPFU	Q4wx15	aspergillus
39	43	52.4	864	1	AGLU_MUCJA	Q92442	mucor javan
40	43	52.4	900	2	Q4LUE0_9BURK	Q4lue0	burkholderi
41	43	52.4	958	1	V1A_CCMV	P27752	cowpea chlo
42	43	52.4	959	2	Q8BEM3_CCMV	Q8bem3	cowpea chlo
43	43	52.4	959	2	Q8BEM6_CCMV	Q8bem6	cowpea chlo
44	43	52.4	1244	2	Q4QII2_LEIMA	Q4qii2	leishmania
45	42.5	51.8	924	1	ORC1_DROME	O16810	drosophila
46	42	51.2	144	2	Q55RY7_CRYNE	Q55ry7	cryptococcu
47	42	51.2	144	2	Q5KGD9_CRYNE	Q5kgd9	cryptococcu
48	42	51.2	166	2	Q19629_CAEEL	Q19629	caenorhabdi
49	42	51.2	185	2	Q19092_CAEEL	Q19092	caenorhabdi
50	42	51.2	226	2	Q4XNH1_PLACH	Q4xnh1	plasmodium
51	42	51.2	245	2	Q4TDT7_TETNG	Q4tdt7	tetraodon n
52	42	51.2	297	2	Q82KH0_STRAW	Q82kh0	streptomyce
53	42	51.2	329	2	Q7Z139_CAEEL	Q7z139	caenorhabdi
54	42	51.2	358	2	Q4RIM3_TETNG	Q4rim3	tetraodon n
55	42	51.2	406	2	Q5B9U0_EMENI	Q5b9u0	aspergillus
56	42	51.2	411	2	Q5UVJ3_STRPU	Q5uvj3	strongyloce
57	42	51.2	414	2	Q4Y2F5_PLACH	Q4y2f5	plasmodium
58	42	51.2	499	2	Q4YB52_PLABE	Q4yb52	plasmodium
59	42	51.2	505	2	Q7RR29_PLAYO	Q7rr29	plasmodium
60	42	51.2	509	2	Q6VGJ5_MAGLA	Q6vgj5	magnolia la
61	42	51.2	557	2	Q9N4H5_CAEEL	Q9n4h5	caenorhabdi
62	42	51.2	594	2	Q8III3_PLAF7	Q8iii3	plasmodium
63	42	51.2	618	2	Q4S5L0_TETNG	Q4s5l0	tetraodon n
64	42	51.2	635	2	Q7YM60_PERA	Q7ym60	persea amer
65	42	51.2	647	2	Q7YM57_9MAGN	Q7ym57	anaxagorea
66	42	51.2	670	2	Q7VZP4_BORPE	Q7vzp4	bordetella
67	42	51.2	670	2	Q7W5B8_BORPA	Q7w5b8	bordetella
68	42	51.2	670	2	Q7WCV0_BORBR	Q7wcv0	bordetella
69	42	51.2	677	2	Q7YM52_9MAGN	Q7ym52	degeneria r
70	42	51.2	682	2	Q7YM50_GALBE	Q7ym50	galbulimima
71	42	51.2	684	2	Q7YM48_MAGTR	Q7ym48	magnolia tr
72	42	51.2	684	2	Q7YM49_LIRCH	Q7ym49	liriodendro